Genetic parameters for a multiple-trait linear model conception rate evaluation

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Background

Nordic Cattle Genetic Evaluation (DK, SWE, FIN)

First common fertility evaluation
for Nordic dairy cattle (2005)

Updated fertility model (2015)

sire model → animal model

repeatability model → multivariate multilactation model

Objectives of the study

Non-return rate ➡ conception rate in the evaluation

Model for variance component estimation needed

Variance components for conception rate

Obstacles of the study

11 complex traits in the same analysis

Modeling conception rate in a multiple trait context

- repeated observations

Sampled data for analyses

Photo:Erkki Oksanen/Luke

From Swedish Red dairy cattle heifers and cows

400 herds with min. 8 first-calvers annually

101 315 females with records
10 397 sires with daughters

Traits

1. **Conception rate** [0 or 1] outcome of each AI

   CR0, CR1, CR2, CR3

   (*heifers, 1st, 2nd and 3rd parity*)

2. **Interval from the first to the last service** [days]

   IFL0, IFL1, IFL2, IFL3

3. **Interval from calving to the first service** [days]

   ICF1, ICF2, ICF3

Model

Multivariate multilactation sire model

- 11 traits: heifers + cows (1. – 3. parities)
- CR as repeated observations within parities, permanent environment as random effect

Model

Fixed effects:

- herd*birth year (heifers) or herd*calving year (cows)
- year-month effect:
  year month of insemination for CR
  year-month of 1st insemination for IFL
  year-month of calving for ICF
- heifers’ first insemination age
- ith insemination for CR

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Model

Fixed effects:

- herd*birth year (heifers) or herd*calving year (cows)
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  year month of insemination for CR
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  year-month of calving for ICF
- heifers’ first insemination age
- ith insemination for CR

Model

Random effects:

- sire
- permanent environment (for all 11 traits)
- residual,
  where residual variances for interval traits were fixed to 2% of the phenotypic variance during REML estimation

Validating ”i^{th} insemination” effect by simulation

Data structure in CR

cow	i^{th} AI	CR
100	1	0
100	2	0
100	3	0
100	4	0
100	5	0
100	6	0
100	7	1

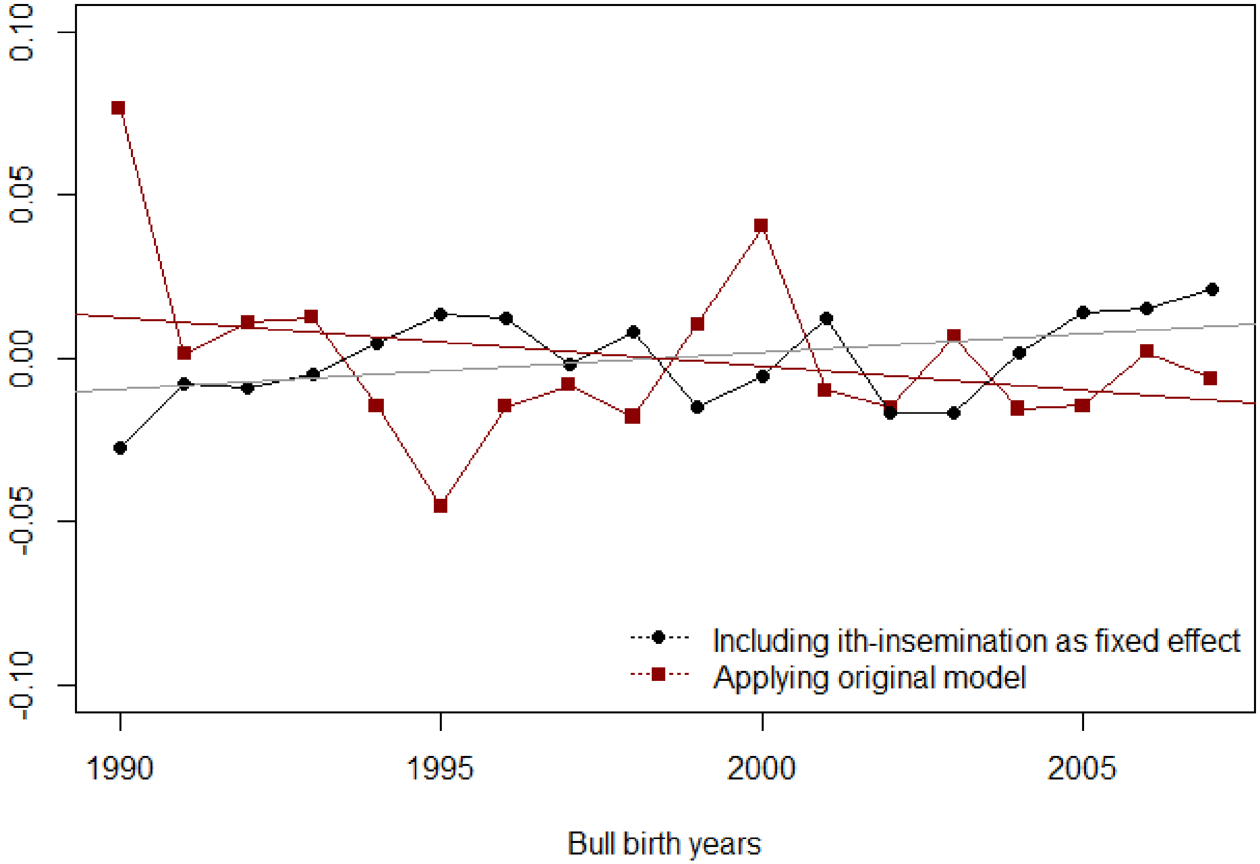
cow	i^{th} AI	CR
101	1	1

cow	i^{th} AI	CR
102	1	0
102	2	1

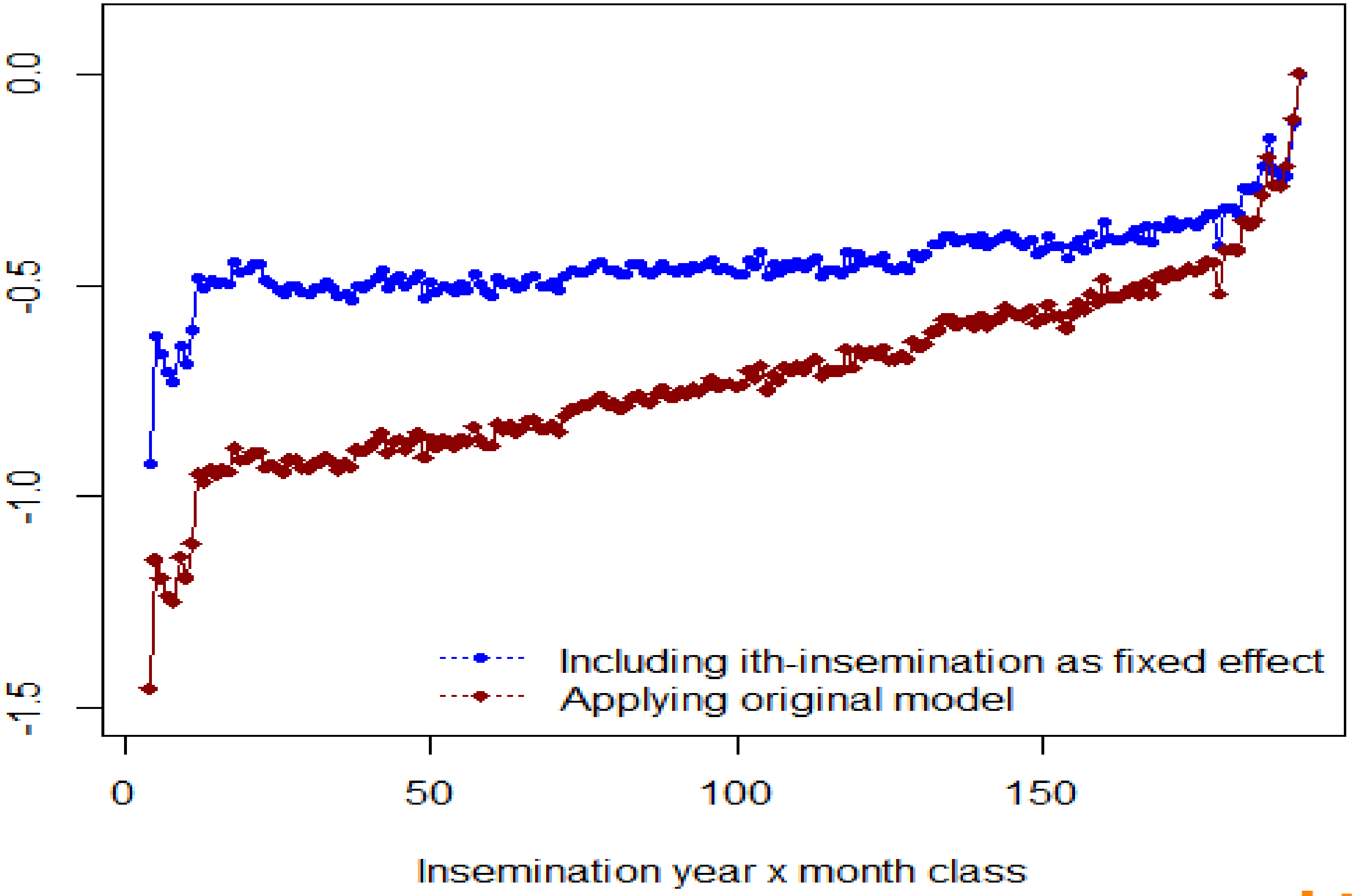
Simulation of conception rate data

- True breeding values & observations simulated for cows with real pedigree
- Based on single trait animal model (h^2=0.1)
- CR observations simulated for observed scale
  - probability of success p=0.6
  - repeated observations until success (max. 10 observations per cow)
- Herd x year and insemination year x month effects simulated to be 0.0
- 5 data replicates

Based on simulation study: genetic trends biased if ith insemination effect excluded



Based on simulation study: environmental trends biased if i^{th} insemination effect excluded



Analyses

- MC-EM REML applied of variance component estimation using the MiX99 software package

Solving Large Mixed Model Equations

VCE results

Heritabilities

	Conception rate	**Interval from first to last AI**	**Interval from calving to first AI**
Heifers	.017	.020	-
1st parity cows	.017	.024	.049
2nd parity cows	.021	.037	.025
3rd parity cows	.024	.041	.032

Genetic and phenotypic correlations within traits: CR


Photo:Erkki Oksanen/Luke

	CR0	CR1	CR2	CR3
CR0		.65	.43	.69
CR1	.03		.90	.95
CR2	.03	.05		.92
CR3	.02	.05	.06	

CR are binomial observations with a variance structure depending on the number of repeated trials service period.

Genetic and phenotypic correlations within traits: ICF


Photo:Erkki Oksanen/Luke

	ICF1	ICF2	ICF3
ICF1		.85	.88
ICF2	.10		.88
ICF3	.08	.11	

Conclusions


Photo:Erkki Oksanen/Luke

- Inclusion of i^{th} insemination is crucial, otherwise
  - h^2 values and genetic correlations inflated
  - trends biased
- Expectation of successful AI affected by the number of previous, unsuccessful AI
- Multiple trait analysis for low-heritable traits was possible

Kaarina Matilainen: ”Single-step genomic evaluation for fertility in Nordic Red Dairy Cattle” EAAP 2016, 31th Aug

Thank you!

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